



results of BLAST

BLASTP 2.2.8 [Jan-05-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1082428074-23889-192291742634.BLASTQ3

Query=

(90 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

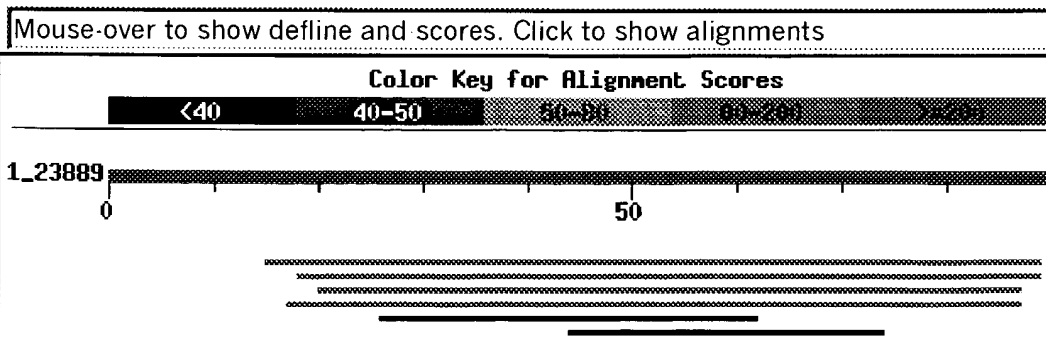
2,768,312 sequences; 778,115,222 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Results of PSI-Blast iteration 1

Taxonomy reports

Distribution of 6 Blast Hits on the Query Sequence



Legend:

- means that the alignment score was below the threshold on the previous iteration
- means that the alignment was checked on the previous iteration

Run PSI Blast iteration 2

Hit list size

Sequences with E-value BETTER than threshold

Sequences producing significant alignments:

	Score	E
		(bits)

<input checked="" type="checkbox"/> <small>NEW</small>	gi 27479893 ref XP_211736.1 	hypothetical protein XP_211736 [Homo sapiens]	145
<input checked="" type="checkbox"/> <small>NEW</small>	gi 37182157 gb AAQ88881.1 	RGPG542 [Homo sapiens]	134
<input checked="" type="checkbox"/> <small>NEW</small>	gi 28204858 gb AAH46522.1 	Unknown (protein for IMAGE:5060814) [...]	132
<input checked="" type="checkbox"/> <small>NEW</small>	gi 41148699 ref XP_372041.1 	similar to RPLK9433 [Homo sapiens] ...	102

Run PSI-Blast iteration 2

Sequences with E-value WORSE than threshold

<input type="checkbox"/>	gi 15602010 ref NP_245082.1 	FtsQ [Pasteurella multocida] >gi 12...	32
<input type="checkbox"/>	gi 16754844 emb CAD10675.2 	Mig1 protein [Debaryomyces occidenta...]	31

Run PSI-Blast iteration 2

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|27479893|ref|XP_211736.1|](#) ☒ hypothetical protein XP_211736 [Homo sapiens]
 Length = 152

Score = 145 bits (367), Expect = 2e-34

Identities = 75/76 (98%), Positives = 75/76 (98%), Gaps = 1/76 (1%)

Query: 16 LGPSPEQRVEIVPRDL-MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCA 74
 LGPSPEQRVEIVPRDL MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCA

Sbjct: 76 LGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCA 135

Query: 75 RLLTRLAVSPVCMEDK 90
 RLLTRLAVSPVCMEDK

Sbjct: 136 RLLTRLAVSPVCMEDK 151


☐ >[gi|37182157|gb|AAQ88881.1|](#) RGPG542 [Homo sapiens]
 Length = 91

Score = 134 bits (338), Expect = 6e-31

Identities = 72/73 (98%), Positives = 72/73 (98%), Gaps = 1/73 (1%)

Query: 19 SPEQRVEIVPRDL-MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLL 77
SPEQRVEIVPRDL MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLL
Sbjct: 19 SPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLL 78





Query: 78 TRLAVSPVCMEDK 90
TRLAVSPVCMEDK
Sbjct: 79 TRLAVSPVCMEDK 91

 >gi|28204858|gb|AAH46522.1| Unknown (protein for IMAGE:5060814) [Mus musculus]
Length = 298

Score = 132 bits (332), Expect = 2e-30
Identities = 67/69 (97%), Positives = 68/69 (98%), Gaps = 1/69 (1%)

Query: 21 EQRVEIVPRDL-MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 79
EQRVEIVPRDL MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
Sbjct: 229 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 288



Query: 80 LAVSPVCME 88
LAVSP+CME
Sbjct: 289 LAVSPMCME 297

 >gi|41148699|ref|XP_372041.1|  similar to RPLK9433 [Homo sapiens]
 gi|37181538|gb|AAQ88580.1|  RPLK9433 [Homo sapiens]
Length = 129

Score = 102 bits (254), Expect = 2e-21
Identities = 51/72 (70%), Positives = 61/72 (84%), Gaps = 1/72 (1%)

Query: 18 PSPEQRVEIVPRDL-MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARL 76
PS + EI PRD +KDKF+KH TGP+ FSP+CSKHFHRLY+NTR+C+ PAYYKRCARL
Sbjct: 57 PSGSRSAEIFPRDSNLKDKFIKHFTGPVTFSPKCSKHFHRLYNTRECSTPAYYKRCARL 116

Query: 77 LTRLAVSPVCME 88
LTRLAVSP+C +
Sbjct: 117 LTRLAVSPLCSQ 128

 >gi|15602010|ref|NP_245082.1| FtsQ [Pasteurella multocida]
 gi|12720362|gb|AAK02229.1| FtsQ [Pasteurella multocida]
Length = 258

Score = 32.3 bits (72), Expect = 3.9
Identities = 14/37 (37%), Positives = 25/37 (67%)

Query: 27 VPRDLMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRD 63
+P D +K+K L HL+GP Y S K + ++++Y N ++
Sbjct: 146 LPFDKLKEKNLPHLSGPDYQSAKVLQAWNQVYLNKE 182

☐ >gi|16754844|emb|CAD10675.2| Mig1 protein [Debaryomyces occidentalis]
Length = 458

Score = 30.8 bits (68), Expect = 9.8

Identities = 16/42 (38%), Positives = 19/42 (45%), Gaps = 11/42 (26%)

Query: 45 YFSPKCSKHFHRLYHNTR-----DCTIPAYYKRCAR 75

Y P C K FHRL H TR CT P +K+ +R

Sbjct: 24 YKCPMCGKAFHRLEHQTRHIRTHTGEKPHSCTFPGCFKKFSR 65

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

Posted date: Apr 19, 2004 3:24 AM

Number of letters in database: 778,115,222

Number of sequences in database: 2,768,312

Lambda	K	H
0.327	0.145	0.469

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 15,201,277

Number of Sequences: 2768312

Number of extensions: 551497

Number of successful extensions: 1261

Number of sequences better than 10.0: 0

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 1261

Number of HSP's gapped (non-prelim): 0

length of query: 90

length of database: 778,115,222

effective HSP length: 59

effective length of query: 31

effective length of database: 614,784,814

effective search space: 19058329234

effective search space used: 19058329234

T: 11

A: 40

X1: 15 (7.1 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

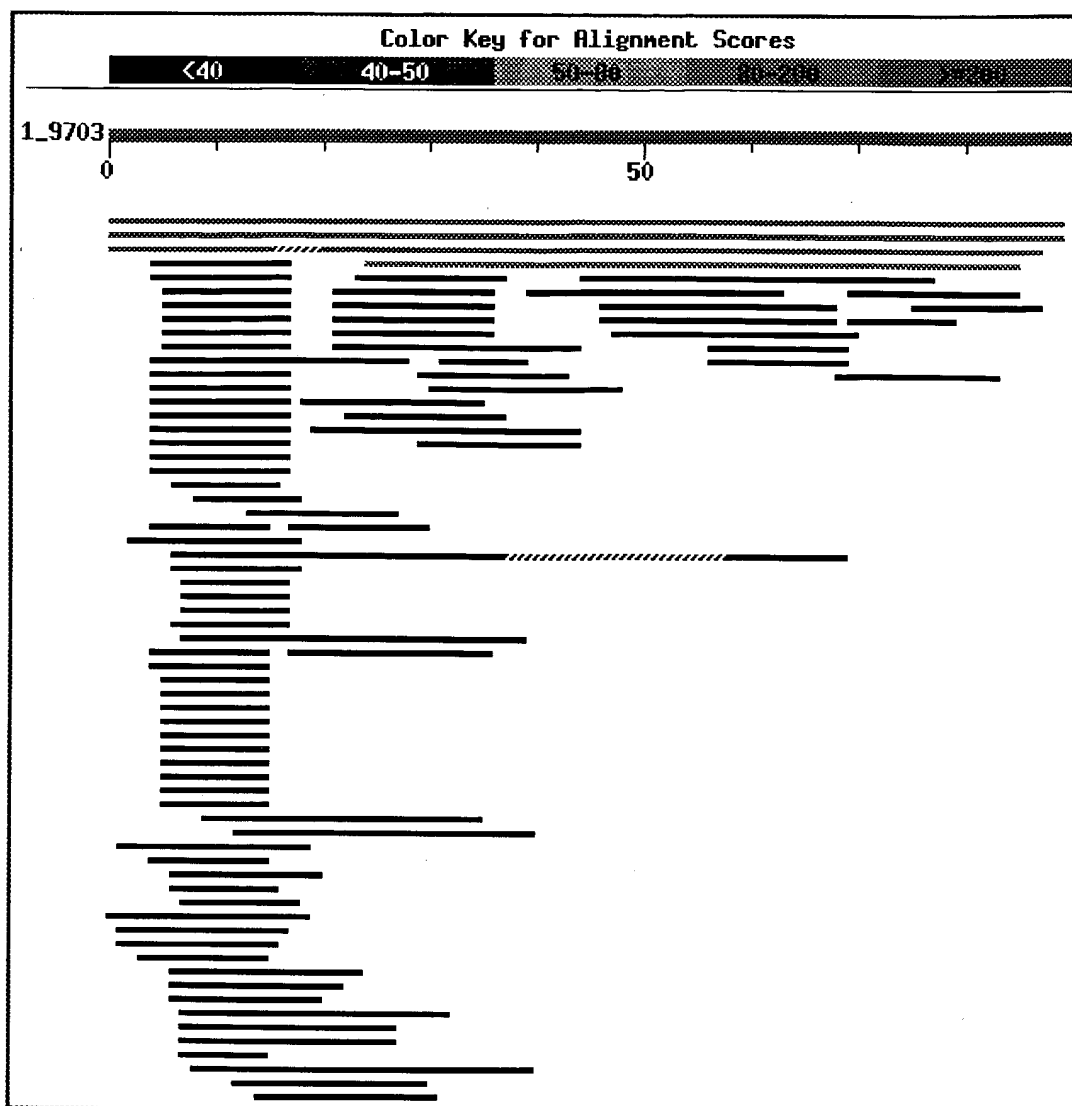
S1: 40 (21.7 bits)

S2: 69 (31.2 bits)

**CDART: Conserved Domain Architecture Retrieval Tool**[New Query](#)[Overview](#)[PubMed](#)[Nucleotide](#)[Protein](#)[Structure](#)[Taxonomy](#)[Help?](#)[About CDART](#)




Sorry, there were no domain hits to your protein. Try increasing the expectation value or turn off low complexity filtering. Some proteins may not have domains defined yet.

[Help](#) | [Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)








Sequences producing significant alignments:

Score E
(bits) Value

gi 37182157 gb AAQ88881.1	RGPG542 [Homo sapiens]	295	7e-79	
gi 27479893 ref XP_211736.1	hypothetical protein XP_211736...	254	1e-66	
gi 28204858 gb AAH46522.1	Unknown (protein for IMAGE:50608...	223	2e-57	
gi 41148699 ref XP_372041.1	similar to RPLK9433 [Homo sapi...	148	1e-34	
gi 6456546 gb AAF09175.1	UDP-glucuronosyltransferase 1A1 [...	37	0.28	
gi 6456548 gb AAF09176.1	UDP-glucuronosyltransferase 1A1 [...	37	0.28	
gi 45199011 ref NP_986040.1	AFR493Cp [Eremothecium gossypi...	37	0.38	
gi 6456554 gb AAF09179.1	UDP-glucuronosyltransferase 1A1 [...	35	1.6	
gi 13641265 gb AAK31597.1	UDP-glucuronosyltransferase UGT1...	35	1.6	
gi 6537144 gb AAF15549.1	UDP-glucuronosyltransferase UGT1A...	35	1.6	
gi 13936939 gb AAK49991.1	UDP-glucuronosyltransferase UGT1...	35	1.6	
gi 6456556 gb AAF09180.1	UDP-glucuronosyltransferase 1A1 [...	35	1.6	
gi 27381266 ref NP_772795.1	ABC transporter ATP-binding pr...	34	2.9	
gi 39998404 ref NP_954355.1	major facilitator family trans...	33	3.9	
gi 13569709 gb AAK31204.1	bilirubin UDP-glucuronosyltrasfer...	32	7.1	
gi 8850236 ref NP_000454.1	UDP glycosyltransferase 1 famil...	32	7.1	

gi 3059177 dbj BAA25600.1	bilirubin UDP-glucuronosyltransf...	32	7.1	
gi 6456550 gb AAF09177.1	UDP-glucuronosyltransferase 1A1 [...	32	7.1	
gi 6010650 gb AAF01205.1	bilirubin UDP-glucuronosyltransfe...	32	7.1	
gi 340132 gb AAA61248.1	bilirubin UDP-glucuronosyltransferase	32	7.1	
gi 12002135 gb AAG43197.1	UDP-glucuronosyltransferase [Hom...	32	7.1	
gi 6456542 gb AAF09173.1	UDP-glucuronosyltransferase 1A1 [...	32	7.1	
gi 15616196 ref NP_244501.1	transcriptional regulator (Ara...	32	9.5	
gi 6009476 dbj BAA84917.1	GfCPS/KS [Gibberella fujikuroi]	32	13	
gi 17367360 sp Q63376 NX2B_RAT	Neurexin 2-beta precursor (N...	32	13	
gi 44240564 gb EAB88833.1	unknown [environmental sequence]	32	13	
gi 11359356 pir JC7227	ent-kaurene synthase - fungus (Gibb...	32	13	
gi 38099400 gb EAA46751.1	hypothetical protein MG10445.4 [...	32	13	
gi 3549899 emb CAA75244.1	copalyl diphosphate synthase [Gi...	32	13	
gi 23063144 ref ZP_00087886.1	hypothetical protein [Pseudo...	32	13	
gi 179419 gb AAA51822.1	beta-galactosidase precursor (EC 3...	31	17	
gi 19745439 ref NP_606575.1	putative ABC transporter (perm...	31	17	
gi 15674485 ref NP_268659.1	putative ABC transporter (perm...	31	17	
gi 21909771 ref NP_664039.1	putative ABC transporter (perm...	31	17	
gi 34328319 ref NP_083633.2	RIKEN cDNA 2010005A06 [Mus mus...	31	17	
gi 21673770 ref NP_661835.1	FecCD transport family protein...	31	17	
gi 46362507 gb AAH66572.1	Unknown (protein for IMAGE:68056...	31	23	
gi 46107834 ref XP_380976.1	hypothetical protein FG00800.1...	31	23	
gi 6456552 gb AAF09178.1	UDP-glucuronosyltransferase 1A1 [...	31	23	
gi 2493675 sp Q28042 OGP_BOVIN	OVIDUCT-SPECIFIC GLYCOPROTEI...	31	23	
gi 43904856 gb EAG06890.1	unknown [environmental sequence]	31	23	
gi 6806893 ref NP_000586.2	lymphotoxin alpha precursor; ly...	30	31	
gi 31880296 gb AAP51424.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 11875697 gb AAG40760.1	urokinase plasminogen activator ...	30	31	
gi 29247065 gb EAA38639.1	GLP_59_9627_8422 [Giardia lambl...	30	31	
gi 31880292 gb AAP51422.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 730164 sp Q02920 NO70_SOYBN	Early nodulin 70 >gi 486678 ...	30	31	
gi 31880318 gb AAP51435.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 31880294 gb AAP51423.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 38106605 gb EAA52893.1	hypothetical protein MG06021.4 [...	30	31	
gi 339743 gb AAB59455.1	tumor necrosis factor-beta	30	31	
gi 31880290 gb AAP51421.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 356345 prf 1209233A	lymphotoxin	30	31	
gi 37213 emb CAA78746.1	lymphotoxin, Tnfb [Homo sapiens] >...	30	31	
gi 11875701 gb AAG40762.1	urokinase plasminogen activator ...	30	31	
gi 43886016 gb EAF96938.1	unknown [environmental sequence]	30	31	
gi 11875699 gb AAG40761.1	urokinase plasminogen activator ...	30	31	
gi 219914 dbj BAA00064.1	lymphotoxin [Homo sapiens] >gi 31...	30	31	
gi 34499061 ref NP_903276.1	conserved hypothetical protein...	30	41	
gi 44316755 gb FAI41271.1	unknown [environmental sequence]	30	41	
gi 11138413 gb AAG31358.1	dipeptidyl carboxy peptidase 1 [...	30	41	
gi 43923909 gb EAG16802.1	unknown [environmental sequence]	30	41	
gi 44348846 gb EAI63835.1	unknown [environmental sequence]	30	41	
gi 46366359 ref ZP_00228687.1	COG1173: ABC-type dipeptide/...	30	41	
gi 42955108 gb EAB44533.1	unknown [environmental sequence]	30	41	
gi 43375113 gb EAD52424.1	unknown [environmental sequence]	30	41	
gi 15612782 ref NP_241085.1	L-lactate permease [Bacillus h...	29	56	
gi 16754844 emb CAD10675.2	Mig1 protein [Debaryomyces occi...	29	56	
gi 26106036 dbj BAC41711.1	poliovirus receptor [Cebus apella]	29	56	
gi 23007557 ref ZP_00049377.1	COG0451: Nucleoside-diphosph...	29	56	
gi 4377961 gb AAD19321.1	pol polyprotein [Human immunodef...	29	56	
gi 6475037 dbj BAA87329.1	sushi-repeat-containing protein ...	29	56	
gi 41199583 ref XP_372161.1	similar to CDNA sequence BC004...	29	56	


gi 34558352 ref NP_908167.1	hypothetical protein WS2068 [W...	29	56	
gi 34873536 ref XP_220919.2	similar to mKIAA1136 protein [...	29	56	
gi 33599656 ref NP_887216.1	putative exported protein [Bor...	29	56	
gi 33595357 ref NP_883000.1	putative exported protein [Bor...	29	56	
gi 18409620 ref NP_566966.1	aspartyl protease family prote...	29	56	
gi 23102087 ref ZP_00088614.1	COG2998: ABC-type tungstate ...	29	56	
gi 16209647 gb AAL14384.1	AT3g52500/F2206_120 [Arabidopsis...	29	56	
gi 23063253 ref ZP_00087995.1	COG2822: Predicted periplasm...	29	56	
gi 4758686 ref NP_002323.1	low density lipoprotein-related...	29	56	
gi 45547567 ref ZP_00187613.1	COG1038: Pyruvate carboxylas...	29	56	
gi 44245170 gb EAA92317.1	unknown [environmental sequence]	29	56	
gi 22973059 ref ZP_00019904.1	hypothetical protein [Chloro...	29	56	
gi 15613532 ref NP_241835.1	SNF2 helicase [Bacillus halodu...	29	56	
gi 42408797 dbj BAD10058.1	putative aminoacylase [Oryza sa...	29	56	
gi 44609104 gb EAK45181.1	unknown [environmental sequence]	29	56	
gi 845468 gb AAA67825.1	precursor protein [Hepatitis C vir...	29	56	
gi 46130328 ref ZP_00165149.2	COG0388: Predicted amidohydr...	29	56	
gi 34557666 ref NP_907481.1	hypothetical protein WS1305 [W...	29	56	
gi 34540006 ref NP_904485.1	hydrolase, carbon-nitrogen fam...	29	56	
gi 43112456 gb EAC22264.1	unknown [environmental sequence]	29	75	
gi 32421455 ref XP_331171.1	hypothetical protein [Neurospo...	29	75	
gi 46099352 gb EAK84585.1	hypothetical protein UM03447.1 [...	29	75	
gi 16552824 dbj BAB71384.1	unnamed protein product [Homo s...	29	75	
gi 18375516 ref NP_542969.1	testicular acid phosphatase is...	29	75	
gi 23104518 ref ZP_00090982.1	COG3204: Uncharacterized pro...	29	75	
gi 40255069 ref NP_653289.2	hypothetical protein FLJ32658 ...	29	75	
gi 34392543 dbj BAC82599.1	reverse transcriptase [Tetraodo...	29	75	

Alignments

Get selected sequences

Select all

Deselect all



 >gi|37182157|gb|AAQ88881.1| RGP542 [Homo sapiens]
Length = 91

Score = 295 bits (688), Expect = 7e-79

Identities = 90/91 (98%), Positives = 90/91 (98%), Gaps = 1/91 (1%)

Query: 1 MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDL-MKDKFLKHLTGPLYFSPKCSKHFHRLYH 59
MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDL MKDKFLKHLTGPLYFSPKCSKHFHRLYH
Sbjct: 1 MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYH 60

Query: 60 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 90
NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK
Sbjct: 61 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 91

 >gi|27479893|ref|XP_211736.1|  hypothetical protein XP_211736 [Homo sapiens]
Length = 152


Score = 254 bits (592), Expect = 1e-66

Identities = 90/151 (59%), Positives = 90/151 (59%), Gaps = 61/151 (40%)

Query: 1 MRGPGHPLL-----LG-----LL-----LV----- 15
 MRGPGHPLL LG LL LV
 Sbjct: 1 MRGPGHPLLLGLLLVLGAAGRGRGGAEPREPADGQALLRLVVELVQELRKHHSAEHKGLQ 60

Query: 16 -----LGPSPEQRVEIVPRDL-MKDKFLKHLTGPLYFSPKCSKHFHRLYH 59
 LGPSPEQRVEIVPRDL MKDKFLKHLTGPLYFSPKCSKHFHRLYH
 Sbjct: 61 LLGRDCALGRAEAAGLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYH 120

Query: 60 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 90
 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK
 Sbjct: 121 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 151

 >gi|28204858|gb|AAH46522.1| Unknown (protein for IMAGE:5060814) [Mus musculus]
 Length = 298




Score = 223 bits (519), Expect = 2e-57
 Identities = 67/69 (97%), Positives = 68/69 (98%), Gaps = 1/69 (1%)

Query: 21 EQRVEIVPRDL-MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 79
 EQRVEIVPRDL MKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
 Sbjct: 229 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 288

Query: 80 LAVSPVCME 88
 LAVSP+CME
 Sbjct: 289 LAVSPMCME 297

Score = 29.9 bits (63), Expect = 41
 Identities = 10/16 (62%), Positives = 12/16 (75%)


Query: 1 MRGPGHPLLLGLLLVL 16
 MR G P+LL LLL+L
 Sbjct: 148 MRVSGRPMLLALLLLL 163

 >gi|41148699|ref|XP_372041.1|  similar to RPLK9433 [Homo sapiens]
 gi|37181538|gb|AAQ88580.1|  RPLK9433 [Homo sapiens]
 Length = 129

Score = 148 bits (342), Expect = 1e-34
 Identities = 50/64 (78%), Positives = 57/64 (89%), Gaps = 3/64 (4%)

Query: 25 EIVPRD--LMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTRLAV 82
 EI PRD L KDKF+KH TGP+ FSP+CSKHFHRLY+NTR+C+ PAYYKRCARLLTRLAV
 Sbjct: 64 EIFPRDSNL-KDKFIKHFTGPTVTFSPKCSKHFHRLYNTRECSTPAYYKRCARLLTRLAV 122

Query: 83 SPVC 86
 SP+C
 Sbjct: 123 SPLC 126

 >gi|6456546|gb|AAF09175.1| UDP-glucuronosyltransferase 1A1 [Gorilla gorilla]
 Length = 25


Score = 37.1 bits (80), Expect = 0.28

Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

GHPL+LGLLL VLGP

Sbjct: 8 GHPLVLGLLLCVLGP 22

 >gi|6456548|gb|AAF09176.1| UDP-glucuronosyltransferase 1A1 [Gorilla gorilla]
Length = 29


Score = 37.1 bits (80), Expect = 0.28

Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

GHPL+LGLLL VLGP

Sbjct: 8 GHPLVLGLLLCVLGP 22

 >gi|45199011|ref|NP_986040.1| AFR493Cp [Eremothecium gossypii]
gi|44985086|gb|AAS53864.1| AFR493Cp [Eremothecium gossypii]
Length = 324


Score = 36.7 bits (79), Expect = 0.38

Identities = 13/18 (72%), Positives = 13/18 (72%), Gaps = 5/18 (27%)

Query: 24 VEIVPRD---LMKDKFLK 38

VEIVPRD LM KFLK

Sbjct: 42 VEIVPRDSPHLM--KFLK 57

 >gi|6456554|gb|AAF09179.1| UDP-glucuronosyltransferase 1A1 [Papio cynocephalus]
Length = 28


Score = 34.6 bits (74), Expect = 1.6

Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18

HPL+LGLLL VLGP

Sbjct: 9 HPLVLGLLLCVLGP 22

 >gi|13641265|gb|AAK31597.1| UDP-glucuronosyltransferase UGT1A01 [Macaca mulatta]
Length = 533

Score = 34.6 bits (74), Expect = 1.6

Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18

HPL+LGLLL VLGP

Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >gi|6537144|gb|AAF15549.1| UDP-glucuronosyltransferase UGT1A01 [Macaca fascicularis]
Length = 533

Score = 34.6 bits (74), Expect = 1.6
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
HPL+LGLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >gi|13936939|gb|AAK49991.1| UDP-glucuronosyltransferase UGT1A01 [Macaca mulatta]
Length = 533

Score = 34.6 bits (74), Expect = 1.6
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
HPL+LGLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >gi|6456556|gb|AAF09180.1| UDP-glucuronosyltransferase 1A1 [Colobus guereza]
Length = 28

Score = 34.6 bits (74), Expect = 1.6
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
HPL+LGLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >gi|27381266|ref|NP_772795.1| ABC transporter ATP-binding protein [Bradyrhizobium
gi|27354433|dbj|BAC51420.1| ABC transporter ATP-binding protein [Bradyrhizobium j
110]
Length = 523

Score = 33.7 bits (72), Expect = 2.9
Identities = 12/17 (70%), Positives = 14/17 (82%), Gaps = 2/17 (11%)

Query: 22 QRVEIVPRDLMKD-KFL 37
QR+EIV R LM+D KFL
Sbjct: 155 QRIEIV-RALMQDPKFL 170

☐ >gi|39998404|ref|NP_954355.1| major facilitator family transporter [Geobacter sulfurreducens]
gi|39985351|gb|AAR36705.1| major facilitator family transporter [Geobacter sulfurreducens]
Length = 414

Score = 33.3 bits (71), Expect = 3.9
Identities = 16/27 (59%), Positives = 17/27 (62%), Gaps = 7/27 (25%)

Query: 5 GHPLLLGLLLV--LGPSPEQRVEIVPR 29

G LLL LLLV LGP+ EQ VPR
 Sbjct: 292 GQSLLLFLLLVLTLGPA-EQ---VPR 313

>[gi|13569709|gb|AAK31204.1|](#) bilirubin UDP-glucuronosyltransferase 1-1 [Homo sapiens]
 Length = 66

Score = 32.5 bits (69), Expect = 7.1
 Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
 G PL+LGLLL VLGP
 Sbjct: 8 GRPLVLGLLLCVLGP 22

>[gi|8850236|ref|NP_000454.1|](#) UDP glycosyltransferase 1 family, polypeptide A1
 bilirubin UDP-glucuronosyltransferase isozyme 1 [Homo sapiens]

[gi|136729|sp|P22309|UD11_HUMAN](#) UDP-glucuronosyltransferase 1-1 precursor, micro
 (UDP-glucuronosyltransferase 1A1) (UDPGT) (UGT1*1)
 (UGT1-01) (UGT1.1) (UGT-1A) (UGT1A) (Bilirubin specific
 UDPGT isozyme 1) (HUG-BR1)

[gi|87534|pir|A39092](#) glucuronosyltransferase (EC 2.4.1.17) 1 precursor,
 bilirubin-specific - human

[gi|184473|gb|AAA63195.1|](#) UDP-glucuronosyltransferase 1

[gi|6094671|gb|AAF03522.1|](#) UDP-glucuronosyltransferase 1 [Homo sapiens]

[gi|11118749|gb|AAG30424.1|](#) UDP glucuronosyltransferase 1A1 [Homo sapiens]

[gi|40849850|gb|AAR95637.1|](#) UDP glycosyltransferase 1 family polypeptide A1 [Homo sapiens]

[gi|742224|prf|2009308A](#) bilirubin UDP glucuronosyltransferase:ISOTYPE=1
 Length = 533

Score = 32.5 bits (69), Expect = 7.1
 Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
 G PL+LGLLL VLGP
 Sbjct: 8 GRPLVLGLLLCVLGP 22

>[gi|3059177|dbj|BAA25600.1|](#) bilirubin UDP-glucuronosyltransferase 1 [Homo sapiens]
 Length = 50

Score = 32.5 bits (69), Expect = 7.1
 Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
 G PL+LGLLL VLGP
 Sbjct: 8 GRPLVLGLLLCVLGP 22

>[gi|6456550|gb|AAF09177.1|](#) UDP-glucuronosyltransferase 1A1 [Pongo pygmaeus]
 Length = 27

Score = 32.5 bits (69), Expect = 7.1
Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
G PL+LGLLL VLGP
Sbjct: 8 GRPLVLGLLLCVLGP 22

>gi|6010650|gb|AAF01205.1| bilirubin UDP-glucuronosyltransferase 1-1 [Homo sapiens]
gi|13448829|gb|AAK27223.1| bilirubin UDP-glucuronosyltransferase 1 [Homo sapiens]
Length = 71

Score = 32.5 bits (69), Expect = 7.1
Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
G PL+LGLLL VLGP
Sbjct: 8 GRPLVLGLLLCVLGP 22

>gi|340132|gb|AAA61248.1| bilirubin UDP-glucuronosyltransferase
Length = 288

Score = 32.5 bits (69), Expect = 7.1
Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
G PL+LGLLL VLGP
Sbjct: 8 GRPLVLGLLLCVLGP 22

>gi|12002135|gb|AAG43197.1| UDP-glucuronosyltransferase [Homo sapiens]
Length = 294

Score = 32.5 bits (69), Expect = 7.1
Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
G PL+LGLLL VLGP
Sbjct: 8 GRPLVLGLLLCVLGP 22

>gi|6456542|gb|AAF09173.1| UDP-glucuronosyltransferase 1A1 [Pan paniscus]
gi|6456544|gb|AAF09174.1| UDP-glucuronosyltransferase 1A1 [Pan troglodytes]
Length = 29

Score = 32.5 bits (69), Expect = 7.1
Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
G PL+LGLLL VLGP
Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >gi|15616196|ref|NP_244501.1| transcriptional regulator (AraC/XylS family) [Bacillus halodurans]
gi|25350122|pir|B84104 transcription regulator (AraC/XylS family) BH3634 [import Bacillus halodurans (strain C-125)]
gi|10176258|dbj|BAB07353.1| transcriptional regulator (AraC/XylS family) [Bacillus halodurans]
Length = 300

Score = 32.0 bits (68), Expect = 9.5
Identities = 16/34 (47%), Positives = 18/34 (52%), Gaps = 8/34 (23%)

Query: 45 YFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLT 78
YF HFHRL+ T CT+ Y KR R LT
Sbjct: 35 YF-----HFHRLFKATVGCTMSEYIKR--RRLT 60

☐ >gi|6009476|dbj|BAA84917.1| GfCPS/KS [Gibberella fujikuroi]
Length = 952

Score = 31.6 bits (67), Expect = 13
Identities = 12/19 (63%), Positives = 14/19 (73%), Gaps = 3/19 (15%)

Query: 22 QRVEIVPRDLMK---DKFL 37
QRVEI PRD +K DK+L
Sbjct: 613 QRVEIYPRDNIKVDEDKYL 631

☐ >gi|17367360|sp|Q63376|NX2B_RAT Neurexin 2-beta precursor (Neurexin II-beta)
gi|1083732|pir|D40228 neurexin II-beta precursor - rat
gi|205719|gb|AAA41708.1| ☐ neurexin II-beta-a [Rattus norvegicus]
Length = 662

Score = 31.6 bits (67), Expect = 13
Identities = 10/11 (90%), Positives = 11/11 (100%)

Query: 7 PLLLGLLLVLG 17
PLLLGLLL+LG
Sbjct: 32 PLLLGLLLLLLG 42

☐ >gi|44240564|gb|EAH88833.1| unknown [environmental sequence]
Length = 107

Score = 31.6 bits (67), Expect = 13
Identities = 11/14 (78%), Positives = 11/14 (78%), Gaps = 1/14 (7%)

Query: 18 PSPEQRVEIVPRDL 31
PS E RV IVPRDL
Sbjct: 15 PS-EDRVSIIVPRDL 27

☐ >gi|11359356|pir|JC7227 ent-kaurene synthase - fungus (Gibberella fujikuroi)
Length = 952



NCBI Conserved Domain Search

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Query= local sequence:
(90 letters)

Database: cdd.v1.65
18,039 PSSMs; 5,506,404 total columns

No hits found ..



...No hits found!

Citing CD-Search: Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen RA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, and Bryant SH (2003), "*CDD: a curated Entrez database of conserved domain alignments*", **Nucleic Acids Res.** 31:383-387.

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Nucleotide

Protein

formatting **BLAST**

Translations

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RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (90 letters)

No putative conserved domains have been detected

The request ID is **1082428074-23889-192291742634.BLASTQ3**

Format!

or

Format!

The results are estimated to be ready in 19 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

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Number of: Descriptions Alignments

Alignment view

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BLAST ☒ with inclusion threshold:

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range: